

What is claimed is:

1. A method for identification of a Gram positive pathogenic organism or a subset of organisms being a member of a predetermined group of pathogenic Gram positive bacteria in a clinical sample comprising
 - a) providing a clinical specimen containing at least partially purified nucleic acid,
 - b) subjecting said clinical specimen to at least one amplification step and at least one detection step, said steps comprising
 - ba) an amplification step using at least one set of amplification primers capable of amplifying a pre-selected nucleic acid sequence region from a predetermined sub-group of pathogenic Gram positive bacteria to which said Gram positive pathogenic organism belongs,
 - bb) a detection step using at least one hybridization reagent capable of detecting said pre-selected nucleic acid sequence region from said predetermined sub-group of pathogenic Gram positive bacteria, said detection step bb) further comprising
 - bba) monitoring hybridization at a pre-selected temperature, said hybridization being indicative for the presence in the sample of at least one species contained in said sub-group, and
 - bbb) monitoring temperature dependence of hybridization, said temperature dependence being indicative for the presence of at least the species of said pathogenic Gram positive bacterium or said subset of organisms,
 - c) identifying said organism or said subset of organisms based on the results of the monitoring steps in bb).
2. A method according to claim 1, wherein said sub-group is a genus.
3. A method according to claim 1, wherein the hybridization reagent comprises two probes complementary to adjacent sequences in the target nucleic acid sequence region, one being labelled by a FRET donor, and the other being labelled by a FRET acceptor.

4. A method according to claim 1, wherein said predetermined group of pathogenic Gram positive bacteria comprises the species *staphylococcus aureus* and coagulase-negative staphylococci.
5. A method according to claim 1, wherein the predetermined subgroup comprises the species *Staphylococcus aureus*, *Streptococcus pneumoniae*, *Enterococcus faecium* and *Enterococcus faecalis*.
6. A method according to claim 1, wherein the preselected nucleic acid sequence region comprises at least 20 nucleotides of an rRNA spacer region.
7. A method according to claim 1, wherein said amplification and detection steps are performed homogeneously.
8. A method according to claim 1, wherein said species are selected from the genera *Staphylococcus*, *Enterococcus* and *Streptococcus*.
9. A method according to claim 1, wherein said species are selected from the genus *Staphylococcus*.
10. A kit for the identification of a Gram positive pathogenic bacterium selected from the genera *Enterococcus*, *Staphylococcus* and *Streptococcus* containing a set of primers capable of amplifying a sequence of at least 20 nucleotides from the 16S-23S rRNA spacer region of *Enterococcus*, *Staphylococcus* or *Streptococcus*.